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OIPE

RAW SEQUENCE LISTING

DATE: 08/01/2003

PATENT APPLICATION: US/10/627,310

TIME: 14:50:04

Input Set : A:\Seqlist.txt

Output Set: N:\CRF4\08012003\J627310.raw

4 <110> APPLICANT: Brooks, Cydney C.
 6 <120> TITLE OF INVENTION: Methods for Treating Diabetes and Insulin resistance
 8 <130> FILE REFERENCE: ADY-009
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/627,310
 C--> 10 <141> CURRENT FILING DATE: 2003-07-25
 10 <150> PRIOR APPLICATION NUMBER: 60/401,389
 11 <151> PRIOR FILING DATE: 2002-08-05
 13 <160> NUMBER OF SEQ ID NOS: 2
 15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 3775
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
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 24 gtggtgaccg tgaggggtgca gtacctggaa gacaccgacc ccttcgcatg tgccaacttt 120
 25 ccggagccgc gccgggcccc cacctgcagc ctggacgggg cgctgccctt gggcgcgag 180
 26 ataccgcggt tgcaccgcct gctgggagcg ccgctcaagt tggaggattg tgctctgcaa 240
 27 gtgtctccct cgggatacta cctggacacc gagctgtccc tggaaagagca gcgggagatg 300
 28 ctggagggct tctatgaaga gatcagcaaa gggcggaagc ccacgctgat ccttcggacc 360
 29 cagctctctg tgaggggtcaa cgctatcttg gaaaagctgt atagctccag tggctcctgag 420
 30 ctccgcgcgt ccctcttctc actgaagcag atcttcagg aggacaaaga cctggtgcct 480
 31 gaatttgtgc attcagaggg gctgagctgc ctgatccgtg tgggtgctgc tgccgaccac 540
 32 aactaccaga gctacatcct tagagcgctc ggccagctga tgctctttgt ggatggaatg 600
 33 ctgggggttg tggccacag tgacactatt cagtggctgt acacattgtg tgccagcctg 660
 34 tcccgccttg tgggtgaagac agccctgaag ctgctgttg tgtttgtaga atactccgaa 720
 35 aacaacgcac cgctgttcat ccgtgcagtg aactctgttg ccacgaccac cgggtgctcct 780
 36 ccctgggcca atctggtgtc cactctggag gagaagaatg gcgctgacct tgagttgttg 840
 37 gtgtacacgg tcacctcat caacaagacg ctggcggcgc tcccggacca ggactccttc 900
 38 tacgatgtga cgatgcact ggagcagcag ggcattggaca cgctggtcca gcgccacctg 960
 39 ggcactgcgg gactgacgt cgacctgcgc acgcagcttg tgctctacga gaacgccctg 1020
 40 aaattggagg atggagacat cgaagaagcc ccaggcgctg gtgggcggcg ggaacgacga 1080
 41 aagccttctt ctgaggagg caagaggagc cgccgttctc tggaaggcgg gggctgcccc 1140
 42 gcgcgtgccc cggaacctgg cccacaggc cccgcctcac cggtaggccc cacctcttcc 1200
 43 accggccccg ccctgctgac agggccccgc tccagccctg tgggcccctc ctccggtctc 1260
 44 caagcttcag tgaacctttt tctaccatc tctgtggcac cctcagctga cacctccagc 1320
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 48 acacccaga gccctgcccc ctgtgtcctg ctccgggccc agcgaagcct tgcaccagag 1560
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ENTERED

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52 ccactgcccc tgctctcggg agtaccccc cctccccac ttccacctcc cccacccatc 1800
53 aaaggccctt tcccaccacc tccacctcta cctctggctg cccctcttcc ccattcagtg 1860
54 cctgacagct cagccctccc cactaagagg aagacagtaa aacttttctg gcgtgacgtg 1920
55 aagctggctg ggggccatgg agtctctgca agccgcttg ggccctgcgc caccctctgg 1980
56 gcttcactgg accctgtctc agtggacacg gcccgactgg aacacctctt tgagtctcgt 2040
57 gccaaagagg tgctgccctc caagaaagct ggagagggcc gccggacaat gaccacagtg 2100
58 ctggacccca agcgcacgaa cgccatcaac atcggcctaa ccacactgcc acctgtgcat 2160
59 gtcattaagg ctgctctgct caactttgat gaggtttctg tcagcaagga tggcattgag 2220
60 aagctactga ccatgatgcc cacggaggaa gagcggcaga agattgaggg agcccagctg 2280
61 gccaaccttg acataccctg gggcccagcc gagaacttcc tgatgactct tgcctccatt 2340
62 ggcggcctcg ctgctcgtct acaactctgg gccttcaagc tggactatga cagcatggag 2400
63 ggggaaattg ctgagccact gtttgacctg aaagtgggta tggacagct ggtacagaat 2460
64 gccaccttcc gctgcatcct ggctaccctc ctagctgtgg gcaacttcct caatggctcc 2520
65 cagagcagcg gctttgagct gagctacctg gagaagggtg cagatgtgaa ggacacggtg 2580
66 cgtcgacagt cactgctaca ccctctctgc tccctagtgc tccagacccg gcctgagtc 2640
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68 ctgactgaga acctggggca gctggagcgc cggagccggg cagccgagga aagcctgcgg 2760
69 agcttgccca agcatgagct ggccccagcc ctgctgccc gcctcacca cttcctggac 2820
70 cagtgtgccc gccgtgttgc catgctaagg atagtgcacc gccgtgtctg caatagggtc 2880
71 catgccttcc tgctctacct gggctacacc ccgagggcg cccgtgaagt gcgcatcatg 2940
72 cagttctgcc acacgctgcg ggaatttgcg cttgagtatc ggacttgccg ggaacgagtg 3000
73 ctacagcagc agcagaagca ggccacatac cgtgagcgca acaagacccg gggacgcatg 3060
74 atcaccgaga cagagaagtt ctcaggtgtg gctggggaag ccccagcaa cccctctgtc 3120
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77 cagagcagct cccaatcat gccacagtg gggccctcca ctgcatcccc agaagaaccc 3300
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79 gtgaccaaga gcagtcctcg tgccttagct gctagggaac gcaagcggtc ccgcggcaac 3420
80 cgcaagtctt tgagaaggac gttgaagagt gggctcggag atgacctggt gcaggcactg 3480
81 ggactaagca agggctctgg cctggagggtg tgaagggtgt gtatcccga aatctatctg 3540
82 gaccctggac tgcagtgcag gagatgacag agtgaggagg gccagagca gaattctggc 3600
83 cccagaactc tgtgccagag agccatgcct tgagcagtat tagccgtgtg tgtatgcatg 3660
84 tgagtgtgtg tgtatgtgtg tgtgtgcatg catatgcatg tgcatgtgtg tgagctcctt 3720
85 gaacgcacgg agcaaaataa aattttctta gctaattccca aaaaaaaaaa aaaaa 3775

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87 <210> SEQ ID NO: 2

88 <211> LENGTH: 1164

89 <212> TYPE: PRT

90 <213> ORGANISM: Homo sapiens

92 <400> SEQUENCE: 2

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93 Met Ala Gly Gly Glu Asp Arg Gly Asp Gly Glu Pro Val Ser Val Val
94 1 5 10 15
95 Thr Val Arg Val Gln Tyr Leu Glu Asp Thr Asp Pro Phe Ala Cys Ala
96 20 25 30
97 Asn Phe Pro Glu Pro Arg Arg Ala Pro Thr Cys Ser Leu Asp Gly Ala
98 35 40 45
99 Leu Pro Leu Gly Ala Gln Ile Pro Ala Val His Arg Leu Leu Gly Ala
100 50 55 60
101 Pro Leu Lys Leu Glu Asp Cys Ala Leu Gln Val Ser Pro Ser Gly Tyr
102 65 70 75 80

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103 Tyr Leu Asp Thr Glu Leu Ser Leu Glu Glu Gln Arg Glu Met Leu Glu
104      85      90      95
105 Gly Phe Tyr Glu Glu Ile Ser Lys Gly Arg Lys Pro Thr Leu Ile Leu
106      100      105      110
107 Arg Thr Gln Leu Ser Val Arg Val Asn Ala Ile Leu Glu Lys Leu Tyr
108      115      120      125
109 Ser Ser Ser Gly Pro Glu Leu Arg Arg Ser Leu Phe Ser Leu Lys Gln
110      130      135      140
111 Ile Phe Gln Glu Asp Lys Asp Leu Val Pro Glu Phe Val His Ser Glu
112 145      150      155      160
113 Gly Leu Ser Cys Leu Ile Arg Val Gly Ala Ala Ala Asp His Asn Tyr
114      165      170      175
115 Gln Ser Tyr Ile Leu Arg Ala Leu Gly Gln Leu Met Leu Phe Val Asp
116      180      185      190
117 Gly Met Leu Gly Val Val Ala His Ser Asp Thr Ile Gln Trp Leu Tyr
118      195      200      205
119 Thr Leu Cys Ala Ser Leu Ser Arg Leu Val Val Lys Thr Ala Leu Lys
120      210      215      220
121 Leu Leu Leu Val Phe Val Glu Tyr Ser Glu Asn Asn Ala Pro Leu Phe
122 225      230      235      240
123 Ile Arg Ala Val Asn Ser Val Ala Thr Thr Thr Gly Ala Pro Pro Trp
124      245      250      255
125 Ala Asn Leu Val Ser Ile Leu Glu Glu Lys Asn Gly Ala Asp Pro Glu
126      260      265      270
127 Leu Leu Val Tyr Thr Val Thr Leu Ile Asn Lys Thr Leu Ala Ala Leu
128      275      280      285
129 Pro Asp Gln Asp Ser Phe Tyr Asp Val Thr Asp Ala Leu Glu Gln Gln
130      290      295      300
131 Gly Met Asp Thr Leu Val Gln Arg His Leu Gly Thr Ala Gly Thr Asp
132 305      310      315      320
133 Val Asp Leu Arg Thr Gln Leu Val Leu Tyr Glu Asn Ala Leu Lys Leu
134      325      330      335
135 Glu Asp Gly Asp Ile Glu Glu Ala Pro Gly Ala Gly Gly Arg Arg Glu
136      340      345      350
137 Arg Arg Lys Pro Ser Ser Glu Glu Gly Lys Arg Ser Arg Arg Ser Leu
138      355      360      365
139 Glu Gly Gly Gly Cys Pro Ala Arg Ala Pro Glu Pro Gly Pro Thr Gly
140      370      375      380
141 Pro Ala Ser Pro Val Gly Pro Thr Ser Ser Thr Gly Pro Ala Leu Leu
142 385      390      395      400
143 Thr Gly Pro Ala Ser Ser Pro Val Gly Pro Pro Ser Gly Leu Gln Ala
144      405      410      415
145 Ser Val Asn Leu Phe Pro Thr Ile Ser Val Ala Pro Ser Ala Asp Thr
146      420      425      430
147 Ser Ser Glu Arg Ser Ile Tyr Lys Ala Arg Phe Leu Glu Asn Val Ala
148      435      440      445
149 Ala Ala Glu Thr Glu Lys Gln Val Ala Leu Ala Gln Gly Arg Ala Glu
150      450      455      460
151 Thr Leu Ala Gly Ala Met Pro Asn Glu Ala Gly Gly His Pro Asp Ala

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152 465          470          475          480
153 Arg Gln Leu Trp Asp Ser Pro Glu Thr Ala Pro Ala Ala Arg Thr Pro
154          485          490          495
155 Gln Ser Pro Ala Pro Cys Val Leu Leu Arg Ala Gln Arg Ser Leu Ala
156          500          505          510
157 Pro Glu Pro Lys Glu Pro Leu Ile Pro Ala Ser Pro Lys Ala Glu Pro
158          515          520          525
159 Ile Trp Glu Leu Pro Thr Arg Ala Pro Arg Leu Ser Ile Gly Asp Leu
160          530          535          540
161 Asp Phe Ser Asp Leu Gly Glu Asp Glu Asp Gln Asp Met Leu Asn Val
162 545          550          555          560
163 Glu Ser Val Glu Ala Gly Lys Asp Ile Pro Ala Pro Ser Pro Pro Leu
164          565          570          575
165 Pro Leu Leu Ser Gly Val Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro
166          580          585          590
167 Pro Ile Lys Gly Pro Phe Pro Pro Pro Pro Pro Leu Pro Leu Ala Ala
168          595          600          605
169 Pro Leu Pro His Ser Val Pro Asp Ser Ser Ala Leu Pro Thr Lys Arg
170          610          615          620
171 Lys Thr Val Lys Leu Phe Trp Arg Asp Val Lys Leu Ala Gly Gly His
172 625          630          635          640
173 Gly Val Ser Ala Ser Arg Phe Gly Pro Cys Ala Thr Leu Trp Ala Ser
174          645          650          655
175 Leu Asp Pro Val Ser Val Asp Thr Ala Arg Leu Glu His Leu Phe Glu
176          660          665          670
177 Ser Arg Ala Lys Glu Val Leu Pro Ser Lys Lys Ala Gly Glu Gly Arg
178          675          680          685
179 Arg Thr Met Thr Thr Val Leu Asp Pro Lys Arg Thr Asn Ala Ile Asn
180          690          695          700
181 Ile Gly Leu Thr Thr Leu Pro Pro Val His Val Ile Lys Ala Ala Leu
182 705          710          715          720
183 Leu Asn Phe Asp Glu Phe Ala Val Ser Lys Asp Gly Ile Glu Lys Leu
184          725          730          735
185 Leu Thr Met Met Pro Thr Glu Glu Glu Arg Gln Lys Ile Glu Gly Ala
186          740          745          750
187 Gln Leu Ala Asn Pro Asp Ile Pro Leu Gly Pro Ala Glu Asn Phe Leu
188          755          760          765
189 Met Thr Leu Ala Ser Ile Gly Gly Leu Ala Ala Arg Leu Gln Leu Trp
190          770          775          780
191 Ala Phe Lys Leu Asp Tyr Asp Ser Met Glu Arg Glu Ile Ala Glu Pro
192 785          790          795          800
193 Leu Phe Asp Leu Lys Val Gly Met Glu Gln Leu Val Gln Asn Ala Thr
194          805          810          815
195 Phe Arg Cys Ile Leu Ala Thr Leu Leu Ala Val Gly Asn Phe Leu Asn
196          820          825          830
197 Gly Ser Gln Ser Ser Gly Phe Glu Leu Ser Tyr Leu Glu Lys Val Ser
198          835          840          845
199 Asp Val Lys Asp Thr Val Arg Arg Gln Ser Leu Leu His His Leu Cys
200          850          855          860

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201 Ser Leu Val Leu Gln Thr Arg Pro Glu Ser Ser Asp Leu Tyr Ser Glu
202 865                               870                               875                               880
203 Ile Pro Ala Leu Thr Arg Cys Ala Lys Val Asp Phe Glu Gln Leu Thr
204                               885                               890                               895
205 Glu Asn Leu Gly Gln Leu Glu Arg Arg Ser Arg Ala Ala Glu Glu Ser
206                               900                               905                               910
207 Leu Arg Ser Leu Ala Lys His Glu Leu Ala Pro Ala Leu Arg Ala Arg
208                               915                               920                               925
209 Leu Thr His Phe Leu Asp Gln Cys Ala Arg Arg Val Ala Met Leu Arg
210                               930                               935                               940
211 Ile Val His Arg Arg Val Cys Asn Arg Phe His Ala Phe Leu Leu Tyr
212 945                               950                               955                               960
213 Leu Gly Tyr Thr Pro Gln Ala Ala Arg Glu Val Arg Ile Met Gln Phe
214                               965                               970                               975
215 Cys His Thr Leu Arg Glu Phe Ala Leu Glu Tyr Arg Thr Cys Arg Glu
216                               980                               985                               990
217 Arg Val Leu Gln Gln Gln Gln Lys Gln Ala Thr Tyr Arg Glu Arg Asn
218                               995                               1000                               1005
219 Lys Thr Arg Gly Arg Met Ile Thr Glu Thr Glu Lys Phe Ser Gly Val
220                               1010                               1015                               1020
221 Ala Gly Glu Ala Pro Ser Asn Pro Ser Val Pro Val Ala Val Ser Ser
222 1025                               1030                               1035                               1040
223 Gly Pro Gly Arg Gly Asp Ala Asp Ser His Ala Ser Met Lys Ser Leu
224                               1045                               1050                               1055
225 Leu Thr Ser Arg Leu Glu Asp Thr Thr His Asn Arg Arg Ser Arg Gly
226                               1060                               1065                               1070
227 Met Val Gln Ser Ser Ser Pro Ile Met Pro Thr Val Gly Pro Ser Thr
228                               1075                               1080                               1085
229 Ala Ser Pro Glu Glu Pro Pro Gly Ser Ser Leu Pro Ser Asp Thr Ser
230                               1090                               1095                               1100
231 Asp Glu Ile Met Asp Leu Leu Val Gln Ser Val Thr Lys Ser Ser Pro
232 1105                               1110                               1115                               1120
233 Arg Ala Leu Ala Ala Arg Glu Arg Lys Arg Ser Arg Gly Asn Arg Lys
234                               1125                               1130                               1135
235 Ser Leu Arg Arg Thr Leu Lys Ser Gly Leu Gly Asp Asp Leu Val Gln
236                               1140                               1145                               1150
237 Ala Leu Gly Leu Ser Lys Gly Pro Gly Leu Glu Val
238                               1155                               1160

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VERIFICATION SUMMARY

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Input Set : A:\Seqlist.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date